



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/671,687
Source: BATCH - RUSH
Date Processed by STIC: 3/29/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable Form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer rejected sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

RECEIVED
APR 20 2001
1600/2000

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/671,687</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted "file", resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

BATCH

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001
TIME: 09:34:53

Input Set : A:\Wallach.app
Output Set: N:\CRF3\03292001\I671687.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: WALLACH, David
4 KOVALENKO, Andrei
5 CANTARELLA, Giuseppina
7 <120> TITLE OF INVENTION: Inhibitor of NF- κ B Activator
9 <130> FILE REFERENCE: WALLACH=25
c. OK 11 <140> CURRENT APPLICATION NUMBER: US/09/671,687
12 <141> CURRENT FILING DATE: 2000-09-28
14 <150> PRIOR APPLICATION NUMBER: PCT/IL99/00158
15 <151> PRIOR FILING DATE: 1999-03-18
17 <150> PRIOR APPLICATION NUMBER: 09/646,403
18 <151> PRIOR FILING DATE: 2000-09-18
20 <150> PRIOR APPLICATION NUMBER: IL 126024
21 <151> PRIOR FILING DATE: 1998-09-01
23 <150> PRIOR APPLICATION NUMBER: IL 134604
24 <151> PRIOR FILING DATE: 2000-02-17
26 <160> NUMBER OF SEQ ID NOS: 4
28 <170> SOFTWARE: PatentIn Ver. 2.0
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 2116
32 <212> TYPE: DNA
33 <213> ORGANISM: HUMAN
35 <400> SEQUENCE: 1
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38 ccaatggaaag tattggccac agtccacttt ctctgtcagc ccagtctgtat atggaagagc 180
39 taaacactgc acccgccaa gagagtccac ccttggccat gcctcctggg aactcacatg 240
40 gtctagaagt gggctcattt gctgaagtta agagagaaccc tcctttctat gggtaatcc 300
41 gttggatcgg tcagccacca ggactgaatg aagtgtctcgc tggactgaa ctggaagatg 360
42 agtgtgcagg ctgtacggat ggaaccttca gaggcactcg gtatttcacc tgtgccctga 420
43 agaaggcgct gtttgtgaaa ctgaagagct gcaggccctga ctcttaggtt gcacattgc 480
44 agccggtttc caatcaagat tgagcgtgt aactcttttag catttggagg ctacttaagt 540
W--> 45 gaagtagtng aagaaaataac tncanccaa aaatggaaaa agaargcttg gagataatga 600
W--> 46 ttggggaaag aagaaaggca tccaaagggtc attacaattc ttgktaactt gnactcaacc 660
W--> 47 ttatctkgc ttatctkgc ttttagttctg ttctinggaca ctgggtgtac ttttagacccc 720
48 aaagaaaaag aaacgtatgtt agaatattwt wkwmimmaccc aagagctact gaggacagaa 780
49 attgttaatc ctctgagaat atatggatat gtgtgtgcca caaaaattat gaaactgagg 840
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51 gaattcttga atattctgtt tcatcatatt ttaagggttag aacctttgtt aaaaataaga 960
52 tcaggaggtc aaaagggtaca agatgttac ttctatcaaa tttttatgg aaaaaatggag 1020
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54 aaatttgcag aggacccatc atgtctgtt attcagatgc ctgcatttgg aaaagacttt 1140
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56 ccccagacag tgccggatat gtggagggtc tgaatgtat gagtgttgaatgatc 1260
57 gatccggaca ccagctggaa aaacaagcag tttttaaaaa cctgcaacac tcaagtccac 1320
58 cttcatccga agaggctgaa tcataaatat aacccagtgt cacttccaa agacttaccc 1380
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60 ctctgcatac aaacaagccaa ctatgttgc tttgtgaatg atggaaagga cgattctgcc 1500

*all item 10 on Error
Summary Sheet*

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Input Set : A:\Wallach.app

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 114 ctgcaggcc t gactctagg t tgcatcatt gcagccggtt tccaatcaga ttgagcgtg 2160
 115 taactctta gcat tttggag gctacttaag tgaagttagta gaagaaaata ctccaccaaa 2220
 116 aatggaaaaa gaaggcttgg agataatgat tgggaagaag aaaggcatcc aggtcatta 2280
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 129 gtcacttccc aaagacttac ccgactggg ctggagacac ggctgcattcc cttgccagaa 3060
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 136 gctggcagtt ctgttcaatgc ccattggccgg caatggatgt ctgttgcgtt atgtccttc 3480
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 138 aacattttg cactctagaa agtatgttt tgttggttt ttaagaagtc taaatgaagt 3600
 139 tattaatacc tgaagctta agttaagtgc attgatcata tgatattttt ggaagcatac 3660
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 143 <211> LENGTH: 949
 144 <212> TYPE: PRT
 145 <213> ORGANISM: HUMAN
 147 <400> SEQUENCE: 3
 148 Met Ser Ser Gly Leu Trp Ser Gln Glu Lys Val Thr Ser Pro Tyr Trp
 149 1 5 10 15
 151 Glu Glu Arg Ile Phe Tyr Leu Leu Leu Gln Glu Cys Ser Val Thr Asp
 152 20 25 30
 154 Lys Gln Thr Gln Lys Leu Leu Lys Val Pro Lys Gly Ser Ile Gly Gln
 155 35 40 45
 157 Tyr Ile Gln Asp Arg Ser Val Gly His Ser Arg Ile Pro Ser Ala Lys
 158 50 55 60
 160 Gly Lys Lys Asn Gln Ile Gly Leu Lys Ile Leu Glu Gln Pro His Ala
 161 65 70 75 80
 163 Val Leu Phe Val Asp Glu Asp Val Val Glu Ile Asn Glu Lys Phe Thr
 164 85 90 95
 166 Glu Leu Leu Leu Ala Ile Thr Asn Cys Glu Glu Arg Phe Ser Leu Phe
 167 100 105 110
 169 Lys Asn Arg Asn Arg Leu Ser Lys Gly Leu Gln Ile Asp Val Gly Cys

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170	115	120	125
172	Pro Val Lys Val Gln Leu Arg Ser Gly Glu Glu Lys Phe Pro Gly Val		
173	130	135	140
175	Val Arg Phe Arg Gly Pro Leu Leu Ala Glu Arg Thr Val Ser Gly Ile		
176	145	150	155
178	Phe Phe Gly Val Glu Leu Leu Glu Gly Arg Gly Gln Gly Phe Thr		160
179	165	170	175
181	Asp Gly Val Tyr Gln Gly Lys Gln Leu Phe Gln Cys Asp Glu Asp Cys		
182	180	185	190
184	Gly Phe Val Ala Leu Asp Lys Leu Glu Leu Ile Glu Asp Asp Asp Thr		
185	195	200	205
187	Ala Leu Glu Ser Asp Tyr Ala Gly Pro Gly Asp Thr Met Gln Val Glu		
188	210	215	220
190	Leu Pro Pro Leu Glu Ile Asn Ser Arg Val Ser Leu Lys Gly Gly Glu		
191	225	230	235
193	Thr Ile Glu Ser Gly Thr Val Ile Phe Cys Asp Val Leu Pro Gly Lys		240
194	245	250	255
196	Glu Ser Leu Gly Tyr Phe Val Gly Val Asp Met Asp Asn Pro Ile Gly		
197	260	265	270
199	Asn Trp Asp Gly Arg Phe Asp Gly Val Leu Cys Ser Phe Ala Cys Val		
200	275	280	285
202	Glu Ser Thr Ile Leu Leu His Ile Asn Asp Ile Ile Pro Glu Ser Val		
203	290	295	300
205	Thr Gln Glu Arg Arg Pro Pro Lys Leu Ala Phe Met Ser Arg Gly Val		
206	305	310	315
208	Gly Asp Lys Gly Ser Ser Ser His Asn Lys Pro Lys Ala Thr Gly Ser		320
209	325	330	335
211	Thr Ser Asp Pro Gly Asn Arg Arg Ser Glu Leu Phe Tyr Thr Leu Asn		
212	340	345	350
214	Gly Ser Ser Val Asp Ser Gln Pro Gln Ser Lys Ser Lys Asn Thr Trp		
215	355	360	365
217	Tyr Ile Asp Glu Val Ala Glu Asp Pro Ala Lys Ser Leu Thr Glu Ile		
218	370	375	380
220	Ser Thr Asp Phe Asp Arg Ser Ser Pro Pro Leu Gln Pro Pro Pro Val		
221	385	390	395
223	Asn Ser Leu Thr Thr Glu Asn Arg Phe His Ser Leu Pro Phe Ser Leu		400
224	405	410	415
226	Thr Lys Met Pro Asn Thr Asn Gly Ser Ile Gly His Ser Pro Leu Ser		
227	420	425	430
229	Leu Ser Ala Gln Ser Val Met Glu Glu Leu Asn Thr Ala Pro Val Gln		
230	435	440	445
232	Glu Ser Pro Pro Leu Ala Met Pro Pro Gly Asn Ser His Gly Leu Glu		
233	450	455	460
235	Val Gly Ser Leu Ala Glu Val Lys Glu Asn Pro Pro Phe Tyr Gly Val		
236	465	470	475
238	Ile Arg Trp Ile Gly Gln Pro Pro Gly Leu Asn Glu Val Leu Ala Gly		480
239	485	490	495
241	Leu Glu Leu Glu Asp Glu Cys Ala Gly Cys Thr Asp Gly Thr Phe Arg		
242	500	505	510

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244 Gly Thr Arg Tyr Phe Thr Cys Ala Leu Lys Lys Ala Leu Phe Val Lys
 245 515 520 525
 247 Leu Lys Ser Cys Arg Pro Asp Ser Arg Phe Ala Ser Leu Gln Pro Val
 248 530 535 540
 250 Ser Asn Gln Ile Glu Arg Cys Asn Ser Leu Ala Phe Gly Gly Tyr Leu
 251 545 550 555 560
 253 Ser Glu Val Val Glu Glu Asn Thr Pro Pro Lys Met Glu Lys Glu Gly
 254 565 570 575
 256 Leu Glu Ile Met Ile Gly Lys Lys Gly Ile Gln Gly His Tyr Asn
 257 580 585 590
 259 Ser Cys Tyr Leu Asp Ser Thr Leu Phe Cys Leu Phe Ala Phe Ser Ser
 260 595 600 605
 262 Val Leu Asp Thr Val Leu Leu Arg Pro Lys Glu Lys Asn Asp Val Glu
 263 610 615 620
 265 Tyr Tyr Ser Glu Thr Gln Glu Leu Leu Arg Thr Glu Ile Val Asn Pro
 266 625 630 635 640
 268 Leu Arg Ile Tyr Gly Tyr Val Cys Ala Thr Lys Ile Met Lys Leu Arg
 269 645 650 655
 271 Lys Ile Leu Glu Lys Val Glu Ala Ala Ser Gly Phe Thr Ser Glu Glu
 272 660 665 670
 274 Lys Asp Pro Glu Glu Phe Leu Asn Ile Leu Phe His His Ile Leu Arg
 275 675 680 685
 277 Val Glu Pro Leu Leu Lys Ile Arg Ser Ala Gly Gln Lys Val Gln Asp
 278 690 695 700
 280 Cys Tyr Phe Tyr Gln Ile Phe Met Glu Lys Asn Glu Lys Val Gly Val
 281 705 710 715 720
 283 Pro Thr Ile Gln Gln Leu Leu Glu Trp Ser Phe Ile Asn Ser Asn Leu
 284 725 730 735
 286 Lys Phe Ala Glu Ala Pro Ser Cys Leu Ile Ile Gln Met Pro Arg Phe
 287 740 745 750
 289 Gly Lys Asp Phe Lys Leu Phe Lys Lys Ile Phe Pro Ser Leu Glu Leu
 290 755 760 765
 292 Asn Ile Thr Asp Leu Leu Glu Asp Thr Pro Arg Gln Cys Arg Ile Cys
 293 770 775 780
 295 Gly Gly Leu Ala Met Tyr Glu Cys Arg Glu Cys Tyr Asp Asp Pro Asp
 296 785 790 795 800
 298 Ile Ser Ala Gly Lys Ile Lys Gln Phe Cys Lys Thr Cys Asn Thr Gln
 299 805 810 815
 301 Val His Leu His Pro Lys Arg Leu Asn His Lys Tyr Asn Pro Val Ser
 302 820 825 830
 304 Leu Pro Lys Asp Leu Pro Asp Trp Asp Trp Arg His Gly Cys Ile Pro
 305 835 840 845
 307 Cys Gln Asn Met Glu Leu Phe Ala Val Leu Cys Ile Glu Thr Ser His
 308 850 855 860
 310 Tyr Val Ala Phe Val Lys Tyr Gly Lys Asp Asp Ser Ala Trp Leu Phe
 311 865 870 875 880
 313 Phe Asp Ser Met Ala Asp Arg Asp Gly Gln Asn Gly Phe Asn Ile
 314 885 890 895
 316 Pro Gln Val Thr Pro Cys Pro Glu Val Gly Glu Tyr Leu Lys Met Ser

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/671,687

DATE: 03/29/2001

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Input Set : A:\Wallach.app

Output Set: N:\CRF3\03292001\I671687.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:45 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:45 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
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L:45 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:45 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:46 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
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L:79 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:79 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:79 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:91 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
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L:101 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
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L:101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2